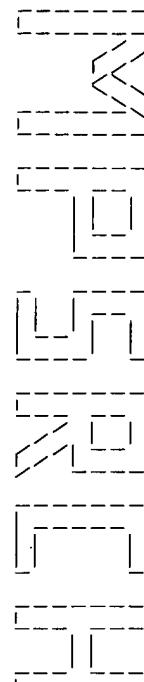


Page 1

 ****  (TM)

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protein - protein database search, using Smith-Waterman algorithm

on: Sat Nov 27 15:32:58 1999; MasPar time 23.10 Seconds
 903.795 Million cell updates/sec

bulbar output not generated.

title: >U5-08-699-716A-2

description: (1-521) from US08699716A.pep

perfect Score: 3546

sequence: 1 MGHHHHHHHHHHSSGHDDD.....RFIQKDSWMQLDDTSGK 521

scoring table: PAM 150

gap 11

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Statistics:						
Post-processing: Minimum Match 0% Listing first 45 summaries						
Database: pir60						
1:pir1 2:pir2 3:pir3 4:pir4						
Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	2245	63.3	326	B33601	lcrV protein - Yersin	0.00e+00
2	2192	61.8	326	B37314	regulatory protein Lc	0.00e+00
3	1100	31.0	170	S13008	capsular antigen F1 p	1.52e-13
4	168	4.7	168	158315	WT1 - human	9.77e-06
5	127	3.6	116	S57382	hypothetical protein	2.34e-01
6	123	3.5	168	A34524	CS3 fimbrial protein	5.77e-01
7	123	3.5	489	S47608	actin homolog YYL081c	5.77e-01
8	124	3.5	857	S33821	median body protein -	4.61e-01
9	123	3.5	2076	S15950	fatty-acyl-CoA synth	5.77e-01
10	120	3.4	220	S484590	hypothetical protein	1.12e+00
11	120	3.4	290	H64591	signal peptidase I -	1.12e+00
12	120	3.4	333	1_KIBYB	ribokinase (EC 2.7.1.	1.12e+00
13	121	3.4	411	158156	Brn-3.2 - mouse	9.01e-01
14	120	3.4	925	T01384	hypothetical protein	1.12e+00
15	119	3.4	2529	A56923	transcription factor	1.40e+00
16	119	3.4	2578	A56922	transcription factor	1.40e+00
17	118	3.3	264	S34121	transcription factor	1.74e+00
18	116	3.3	373	S76273	hypothetical protein	2.69e+00
19	118	3.3	410	I38502	gene Brn-3b protein -	1.74e+00
20	116	3.3	650	S41481	DNA-directed RNA poly	2.69e+00
21	117	3.3	1302	JC6009	surface-located membr	2.17e+00
22	112	187	2	G70406	suroheme synthase - A	6.31e+00
23	112	3.2	290	D71921	signal peptidase I -	6.31e+00

RESULT 2 B37314 #type complete
ENTRY regulatory protein Lcrv - *Yersinia pseudotuberculosis*
TITLE #formal_name *Yersinia pseudotuberculosis*
ORGANISM #accessions
DATE 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change
17-Mar-1999

B37314 Analysis of the V antigen lcrGVH-yopBD operon of *Yersinia pseudotuberculosis*: evidence for a regulatory role of Lcrv and Lcrv.

#journal J. Bacteriol. (1991) 173:1607-1616
Bergman, T.; Hakansson, S.; Forsberg, A.; Norlander, L.; Macellaro, A.; Baekman, A.; Boelin, I.; Wolf-Watz, H.

#cross-references MUID:91154114

#accession B37314
##status Preliminary
##molecule_type DNA
##residues 1-326 #label BER

##cross-references GB: M57893; NID: 915456; PID: 9155458

SUMMARY #length 326 #molecular-weight 37336 #checksum 4689

Query Match Best Local Similarity 61.8%; Score 2192; DB 2; Length 326;
Matches 315; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Db 1 MIRAYEQNPQHFIQDELEKVRVQEQLTGHGSVSYLELQVYKDKNIDISKYDPRKSEVFA 60
Qy ||||||| MIRAYEQNPQHFIQDELEKVRVQEQLTGHGSVSYLELQVYKDKNIDISKYDPRKSEVFA 255

Db 61 NRVITDIELKKILAYFLPEDAIIKGHDNQLONGIKRVEKLESPNTQWEIRAFMA 120
Qy ||||| NRVITDIELKKILAYFLPEDAIIKGHDNQLONGIKRVEKLESPNTQWEIRAFMA 315

Db 121 VHFSTIADRIIDDKLKVIVDMSMHGDAKSRLBLAELTAELAKIYVQAEINKHSS 180
Qy 316 VMHFSLTADRIIDDKLKVIVDMSMHGDAKSRLBLAELTAELAKIYVQAEINKHSS 375

Db 181 GGTINIHDKSINLMKRNLYGCTDEELFKASAEYKLEKMPQTTOEGEERKTIKVNFL 240
Qy ;||||| GGTINIHDKSINLMKRNLYGCTDEELFKASAEYKLEKMPQTTOEGEERKTIKVNFL 376

Db 241 ESEKRTGALGNLKSYSYNNKDNELSHFATCSDSKRPLNDLVSQKTTQLDTSRFNS 300
Qy |||:||||| ESEKRTGALGNLKSYSYNNKDNELSHFATCSDSKRPLNDLVSQKTTQLDTSRFNS 495

Db 301 AIEALNRFIQLYDSMQRLLDDTSK 326
Qy 496 AIEALNRFIQLYDSMQRLLDDTSK 521

RESULT 3 S13008 #type complete
ENTRY capsular antigen F1 precursor - *Yersinia pestis*
TITLE #formal_name *Yersinia pestis*
ORGANISM DATE 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change
13-Sep-1998

S13008 #accessions
#reference
#authors Galyov, E.E.; Smirnov, O.Y.; Karlishev, A.V.; Volkovoy, K.I.; Denesruk, A.I.; Nazimov, I.V.; Rubtsov, K.S.; Abramov, V.M.; Dalvadyan, S.M.; Dav'yaylov, V.P.

FEMS Lett. (1990) 277:230-232

#journal Nucleotide sequence of the *Yersinia pestis* gene encoding F1 antigen and the primary structure of the protein. Putative T and B cell epitopes.

#cross-references MUID: 9109503

#accession S13008
##molecule_type DNA
##residues 1-170 #label GAL

##cross-references EMBL: X61996; NID: 948620; PID: 948621

RESULT 4 158315 #type complete
ENTRY WT1 - human
TITLE #formal_name Homo sapiens #common_name man
ORGANISM DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
29-Aug-1997

ACCESSIONS 158315

REFERENCE 158315
#authors Hamilton, T.B.; Barilla, K.C.; Romaniuk, P.J.
#journal Nucleic Acids Res. (1995) 23:277-284

#cross-references MUID: 95166649

#accession 158315

##status Preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
##residues 1-168 #label RES
#title High affinity binding sites for the Wilms' tumour suppressor protein WT1.

GENETICS #cross-references GB:S75264; NID: 9896246; PID: 9896247

##accession 158315

##molecule_type mRNA
##residues 1-168 #label RES
#title High affinity binding sites for the Wilms' tumour suppressor protein WT1.

Query Match Best Local Similarity 47%; Score 168; DB 2; Length 168;
Matches 20; Conservative 7; Mismatches 1; Indels 2; Gaps 1;

Db 1 MGHHHHHHHHHSSCHIEG--RHMRRVPGV 28
Qy 1 MGHHHHHHHHSSGHDDDKHMKKISSY 30

RESULT 5 S57382 #type complete
ENTRY hypothetical protein YOL087c - yeast (Saccharomyces cerevisiae)
TITLE ALTERNATE NAMES hypothetical protein 00944
ORGANISM #formal_name *Saccharomyces cerevisiae*
DATE 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
12-Dec-1997

ACCESSIONS S57382; S66781; S50418
REFERENCE S57374

#authors Zunstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.

#journal Yeast (1995) 11:975-986

#title A 29.425 kb segment on the left arm of yeast chromosome XV contains more than twice as many unknown as known open

reading frames.

#cross-references MUID:96021609

#accession S57382

#status nucleic acid sequence not shown

#molecule_type DNA

#residues 1-1116 #label ZUM

REFERENCE S66775

#authors Zumstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.

#submision submitted to the Protein Sequence Database, July 1996

#accession S66781

#molecule_type DNA

#residues 1-1116 #label ZUW

#cross-references EMBL:Z14829; NID:91419927; PID:e251885; PID:91419928; MIPS:Y01087C

#experimental_source strain S28C

GENETICS

#map_position 15L #length 1116 #molecular-weight 125381 #checksum 1996

SUMMARY

Query Match 3.5%; Score 133; DB 2; Length 158;

Best Local Similarity 23.5%; Pred. No. 5.77e-01;

Matches 40; Conservative 48; Mismatches 72; Indels 10; Gaps 10;

Matches 16; Conservative 21; Mismatches 24; Indels 1; Gaps 1;

Db 1 MIRKLYLILGLSLSAMSSYAAAGPPLIKTELALNVSPAAQDATWAPQDNUTLSNG-V 59

Qy 24 MKKISSV-IAIAFLGFTIA-TANRADLTASTATATVEPARILITKEGARITIMONGNI 81

Db 60 -SNTLVAVLTSNTSDTIVSASTSYSDTSKNGT-VFAHATNNASFAT-ISTDNANI 116

Qy 82 DTEFLLVGLTIGGYKIGTS-TSVNFIDAGDPMLTFSQDGNNHOFTTIVKGDSRDF 140

Db 117 TLD-KNAGNTIV-KTNGSQLPNTNLPLKFITEGNEHLVSNYRANIT 164

Qy 141 DISPKVNGENVGDDVVATGSDFFVRSIGSKGGK-LAAGKYTDATVVT 189

RESULT 6

ENTRY a34952 #type complete

TITLE CS3 fimbrial protein precursor - Escherichia coli

ALTERNATE_NAMES CS3 pilin

ORGANISM #formal_name Escherichia coli

DATE 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change

ACCESSIONS S47608; S56029; S56858; S37563

REFERENCE 47608

#authors Wintersberger, U.

#submision submitted to the EMBL Data Library, December 1993

#accession S47608

#molecule_type DNA

#residues 1-489 #label WIN

#cross-references EMBL:X75317; NID:9436807; PID:9436808

REFERENCE S56016

#authors Miosga, T.; Schaaff-Gerstenschlaeger, I.; Chalwatzzis, N.; Baur, A.; Boles, E.; Fournier, C.; Schmitt, S.; Velten, C.; Wilhelm, N.; Zimmermann, F.K.

#journal Yeast (1995) 11:681-689

#title Sequence analysis of a 33.1 kb fragment from the left arm of Saccharomyces cerevisiae chromosome X, including putative proteins with leucine zippers, a fungal Zn(II)2-CS(6) binuclear cluster domain and a putative alpha-2-SCB-alpha-2 binding site.

#cross-references MUID:96093911

#accession S56029

#status nucleic acid sequence not shown; translation not shown

#molecule_type DNA

#residues 1-489 #label MTO

#cross-references EMBL:X33502; NID:9929861; PID:9929875

#note the nucleotide sequence was submitted to the EMBL Data Library, December 1994

REFERENCE S56855

#authors Miosga, T.; Schaaff-Gerstenschlaeger, I.; Baur, A.; Boles, E.; Chalwatzzis, N.; Fournier, C.; Schmitt, S.; Velten, C.; Wilhelm, N.; Witzel, A.; Zimmermann, F.K.

#accession S56858

#submision submitted to the Protein Sequence Database, September 1995

#cross-references EMBL:Z49356; NID:91008243; PID:91008244; MIPS:YJL081C

GENETICS

#gene SGD:ARP4; ACT3

#cross-references MIPS:YJL081C; SGD:S0003617

#map_position 10L

CLASSIFICATION superfamily actin

KEYWORDS cytoskeleton

SUMMARY #length 489 #molecular-weight 54831 #checksum 8019

FEATURE 1-22

#domain signal sequence #status predicted #label SIGN

#product CS3 fimbrial protein #status experimental

#label MAT

SUMMARY #length 168 #molecular-weight 17464 #checksum 9103

Query Match 3.5%; Score 123; DB 2; Length 489;

Best Local Similarity 25.8%; Pred. No. 5.77e-01;

Matches 16; Conservative 21; Mismatches 24; Indels 1; Gaps 1;

Db 22 GSYTNTGYSGSFPOSTLPSYKGKTADEGKMKKISEQSGIPRKDYLEPLIE-NGIV 80

RESULT 15
 ENTRY A56923 #type complete
 TITLE transcription factor shn - fruit fly (Drosophila
 melanogaster)
 ALTERNATE NAMES schnurri
 ORGANISM #formal_name Drosophila melanogaster
 DATE 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change
 17-Mar-1999
 ACCESSIONS A56923
 REFERENCE A56923
 #authors Grieder, N.C.; Nellen, D.; Burke, R.; Basler, K.; Affolter, M.
 #journal Cell (1995) 81:711-800
 #title schnurri is required for Drosophila Dpp signaling and encodes a zinc finger protein similar to the mammalian transcription factor PRO11-BFI.
 #cross-references MUID:95292346
 #accession A56923
 #status preliminary; nucleic acid sequence not shown; not
 compared with conceptual translation
 #molecule_type mRNA
 #residues 1-2529 #label GRI
 #cross-references GB:L42311
 GENETICS
 #gene FlyBase:shn
 #cross-references FlyBase:FBgn0003395
 KEYWORDS DNA binding; transcription factor; zinc finger
 SUMMARY #length 2529 #molecular_weight 271637 #checksum 9689
 Query Match 3.4%; Score 119; DB 2; Length 2529;
 Best Local Similarity 24.6%; Pred. No. 1.40e+00;
 Matches 32; Conservative 38; Mismatches 55; Indels 5; Gaps 5;
 Db 30 ATAAAAAAAATTVTATPKKR-TYRETTATTVTQRSENKANAAATAAATTA 88
 Qy 38 TIATANAADLTASTATATLVEPARITYKEGAPITIMDNGNTDELYGLLGGYKT 97
 Db 89 ATASASASATATATAT-LT-ASKAATAATTAAGASGNNSSSKPSSTRDKI-GE-VP 144
 Qy 98 GTTTSVNTDASDPMYLFTSDQGNNOFTTIVKGKDSRDFDISPKNGENIVGDDV 157
 Db 145 LPTVDSNHII 154
 Qy 158 LATQSQDFV 167
 Search completed: Sat Nov 27 15:34:00 1999
 Job time : 62 secs.

QY 256 NRVTDDIELKKILAYLPEDEALKGHDNOLONGIKRKFLESSPNTQWELRMA 315
 QY 256 NRVTDDIELKKILAYLPEDEALKGHDNOLONGIKRKFLESSPNTQWELRMA 315
 Db 121 VMHFSLTADRIDDVLYKVTDSMNNHGDARKLREELAELTAELKIVSQAENKHLSS 180
 QY 316 VMHFSLTADRIDDVLYKVTDSMNNHGDARKLREELAELTAELKIVSQAENKHLSS 375
 Db 181 SGTNINHKSSINLMDKNLYGYTDEEIKASAEXKILEKMPQTAIQDSEKKIVSKDFL 240
 QY 376 SGTNINHKSSINLMDKNLYGYTDEEIKASAEXKILEKMPQTAIQDSEKKIVSKDFL 435
 Db 241 GSENKRTGALGNLKNSSYSYNKNDNELSHAFATCSDKSRLPLNDLVSQKTLSDITSRENS 300
 QY 436 GSENKRTGALGNLKNSSYSYNKNDNELSHAFATCSDKSRLPLNDLVSQKTLSDITSRENS 495
 Db 301 ATEALNRFTQKYDSVMORLDDTSKG 326
 QY 496 ATEALNRFTQKYDSVMORLDDTSKG 521

RESULT 2
 ID LCRY_YERV STANDARD; PRT; 326 AA.
 AC P23994;
 DT 01-MAR-1992 (REL. 21, CREATED)
 DT 01-NOV-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DE VIRULENCE-ASSOCIATED V ANTIGEN (LOW CALCIUM RESPONSE LOCUS PROTEIN V).
 DE LCRV.
 GN YERSINIA_PSEUDOTUBERCULOSIS.
 OS PLASMID FIBI.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
 OC YERSINIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN YPIII.
 RX MEDLINE: 91164114.
 RA BERGMAN T., HAKANSSON S., FORSSBERG A., NORLANDER L., MACELIARO A.,
 RA BAECKMAN A., BOELLIN I., WOLF-WATZ H.;
 RT "Analysis of the V antigen lcrGvH-yopB operon of Yersinia pseudotuberculosis: evidence for a regulatory role of lcrH and lcrV.";
 RT J. BACTERIOL. 173:1607-1616(1991).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP ROGGENKAMP A., HESEMMANN J.;
 RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -!- FUNCTION: INVOLVED IN CA(2+) REGULATION OF YOP EXPRESSION, WHICH
 CC INCLUDES THE EXPORT PROCESS.
 CC -!- SUBCELLULAR LOCATION: SECRETED.

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 CC -----
 DR EMBL: M57893; G155458; -;
 DR EMBL: X66802; E23989; -;
 DR PIR: B37314; B37314.
 DR SEQUENCE 326 AA; 37336 MW; 7D84E243 CRC32;
 KW PLASMID; ANTIGEN; VIRULENCE.
 SQ Query Match 61.8%; Score 219; DB 1; Length 326;
 Best Local Similarity 96.6%; Pred. No. 0.00e+00; Mismatches 4; Indels 0; Gaps 0;
 Matches 315; Conservative 7;
 DR MIRAYEQNQHFDDELEKRVQEQTGHHGSVLEFLVQVKDQUDISIYDPRKSEVFA 60
 DR MIRAYEQNQHFDDELEKRVQEQTGHHGSVLEFLVQVKDQUDISIYDPRKSEVFA 255
 QY 196 MIRAYEQNQHFDDELEKRVQEQTGHHGSVLEFLVQVKDQUDISIYDPRKSEVFA 255

RESULT 3
 ID CAFL_YERPE STANDARD; PRT; 170 AA.
 AC P26048;
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
 DE F1 CAPSULE ANTIGEN PRECURSOR.
 DE CAFL.
 GN YERSINIA_PESTIS.
 OS PLASMID PFRA.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
 OC YERSINIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 9109503.
 RX GAL'KOV E. E., SMIRNOV O. Y., KARLISHEV A. V., VOLKOVY K. I.,
 RA DANILOV A. I., NAJIMOV I. V., RUSTOV K. S., ABRAMOV V. M.,
 RA DALVADYAN S. M., ZAV'YALOV V. P.;
 RT "Nucleotide sequence of the Yersinia pestis gene encoding F1 antigen and the primary structure of the protein. Putative T and B cell epitopes"; FEBS LETT. 277:230-232(1990).
 RT RL [2]
 CC -!- SUBCELLULAR LOCATION: CAPSULE.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X61996; G48621; -.
 DR PIR: S13008; S13008.
 KW PLASMID; SIGNAL.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 170 F1 CAPSULE ANTIGEN.
 FT DOMAIN 100 150 CONTAINS POTENTIAL ANTIGENIC DETERMINANTS
 FT THAT MAY STIMULATE T-CELLS.
 SQ SEQUENCE 170 AA; 1766 MW; 35432B5 CRC32;

Query Match 31.0%; Score 110; DB 1; Length 170;
 Best Local Similarity 100.0%; Pred. No. 5.16e-166; Mismatches 170; Conservative 0; Indels 0; Gaps 0;
 Matches 170; Conservative 0;
 DR 1 MKKISSVIALFGTATANADLTASTATIAALVPEARTITYKECAPITMDNGID 60
 DR 24 MKKISSVIALFGTATANADLTASTATIAALVPEARTITYKECAPITMDNGID 83
 DR 61 ELVGTGLTGGYKTGTTSTVNPETDAAGDPMLTFSODGNHOOFTTKVQKDSRFD 120
 QY 84 ELLVGTGLTGGYKTGTTSTVNPETDAAGDPMLTFSODGNHOOFTTKVQKDSRFD 143

RT	developmental control genes";
CC	CYTOKINETIC CELL GENET. 66:267-271(1994).
CC	-!- FUNCTION: MAY PLAY A ROLE IN DETERMINING OR MAINTAINING THE IDENTITIES OF A SMALL SUBSET OF VISUAL SYSTEM NEURONS.
CC	-!- SUBCELLULAR LOCATION: NUCLEAR.
CC	-!- TISSUE SPECIFICITY: BRAIN, PERIPHERAL SENSORY NERVOUS SYSTEM AND RETINA. IN THE ADULT NERVOUS SYSTEM BRY-3.2 PREDOMINATES IN THE OPTICAL, INTERMEDIATE, AND DEEP GRAY AREAS OF THE SUPERIOR OPTICUS, THE DORSAL COLUMN OF THE MESENCEPHALIC AND PONTINE CENTRAL GRAY AND THE LATERAL INTERPEDUNCULAR NUCLEUS.
CC	-!- DEVELOPMENTAL STAGE: IN THE CNS IT IS SELECTIVELY EXPRESSED IN POSTMITOTIC, TERMINALLY DIFFERENTIATED NEURONS.
CC	-!- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS TO CLASS 4 POU.
CC	-----
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CC	-----
CC	EMBL: S68377; G545069; -.
DR	EMBL; S69351; G56434; -.
DR	MGDB: M32524; POU4F2.
DR	PS0027; HOMEOBOX_1; 1.
DR	PROSITE; PS0035; POU_1; 1.
DR	PROSITE; PS00465; POU_2; 1.
DR	PROSITE; PS0071; HOMEOBOX_2; 1.
DR	PFAM; PF00046; homeobox; 1.
DR	PFAM; PF00157; pou; 1.
DR	HSSP; P10037; 1AU7.
FT	NUCLEAR PROTEIN; DNA-BINDING; HOMEOBOX.
FT	DOMAIN 1 4 POLY-MET.
FT	DOMAIN 43 51 POLY-SER.
FT	DOMAIN 54 67 POLY-GLY.
FT	DOMAIN 69 77 POLY-SER.
FT	DOMAIN 76 85 POLY-GLY.
FT	DOMAIN 112 121 POU-IV BOX.
FT	DOMAIN 128 131 POLY-HIS.
FT	DOMAIN 157 160 POLY-SER.
FT	DOMAIN 173 184 POLY-HIS.
FT	DOMAIN 255 329 POU DOMAIN.
FT	DNA-BIND 347 406 HOMEOBOX.
FT	CONFLICT 90 98 RRAAGLIPPP -> MCAYFYIQLQ (IN REF. 2).
FT	CONFLICT 404 405 RM -> KV (IN REF. 2).
SQ	SEQUENCE 411 AA; 43172 MW; 99973657 CRC32;
Query Match	3.4%; Score 121; DB 1; Length 411;
Best Local Similarity	28.6%; Pred. No. 1.56e-01; Length 411;
Matches	24; Conservative 22; Mismatches 35; Indels 3; Gaps 3;
Db	174 HHHHHHHHHHHHQHQALEGELLEHLHSPGIALGAMAGPDCTVSTPAHMHMTMPMHQA 233
Qy	3 HHHHHHHHHSSGHIDDDDKHMKRKKISSVTAI-ALFGTIATANADLTASTTATLVERA 61
Db	234 AISMWAHGLP-SHMGCMSSDVAD 256
Qy	62 RILTYKEGGAPITMD-NGNIDTE 84
RESULT	11
ID	BRY-3_HUMAN STANDARD; PRT; 410 AA.
AC	Q12837; Q13983; Q14987;
DT	01-NOV-1997 (REL. 35, CREATED)
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE	BRAIN-SPECIFIC HOMEOBOX/POU DOMAIN PROTEIN 3B (BRN-3B).
OS	HOMO SAPIENS (HUMAN).
GN	POU4F2 OR BRY3B.
OC	EUKARYOTA; METAZOA; CHORDATA; MAMMALIA; EUTHERIA; PRIMATES; CAVIARHINI; HOMINIDAE; HOMO.
RN	[1] SEQUENCE FROM N.A.
RP	TISSUE=RETINA;
RC	RX MEDLINE; 94000832.
RA	XIANG M., ZHOU L.-J., PENG Y., EDDY R.L., SHOWS T.B., NATHANS J.;
RT	"Brn-3b: a POU domain gene expressed in a subset of retinal ganglion cells." [2] NEURON 11:689-701(1993).
RT	SEQUENCE OF 146-410 FROM N.A.
RC	SEQUENCE OF 275-392 FROM N.A.
RX	RT TISSUE=TESTIS;
RA	RING C.J.A., LATCHMAN D.S.;
RT	"The human Brn-3b POU transcription factor shows only limited homology to the Brn-3a/RDC-1 factor outside the conserved POU domain." [3] NEURON 11:689-701(1993).
RL	SEQUENCE OF 275-392 FROM N.A.
RT	RT JURKAT T cells." [3] NEURON 11:689-701(1993).
RL	PROC. NATL. ACAD. SCI. U.S.A. 90:10260-10264(1993).
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CC	-----
CC	EMBL: M32524; POU4F2.
DR	PS0027; HOMEOBOX_1; 1.
DR	PROSITE; PS0035; POU_1; 1.
DR	PROSITE; PS00465; POU_2; 1.
DR	PROSITE; PS0071; HOMEOBOX_2; 1.
DR	PFAM; PF00046; homeobox; 1.
DR	PFAM; PF00157; pou; 1.
DR	HSSP; P10037; 1AU7.
FT	NUCLEAR PROTEIN; DNA-BINDING; HOMEOBOX.
FT	DOMAIN 1 4 POLY-MET.
FT	DOMAIN 43 51 POLY-SER.
FT	DOMAIN 54 67 POLY-GLY.
FT	DOMAIN 71 80 POLY-SER.
FT	DOMAIN 81 84 POLY-GLY.
FT	DOMAIN 111 120 POU-IV BOX.
FT	DOMAIN 127 130 POLY-HIS.
FT	DOMAIN 156 159 POLY-SER.
FT	DOMAIN 172 183 POLY-HIS.
FT	DOMAIN 254 328 POU DOMAIN.
FT	DNA-BIND 346 405 HOMEOBOX.
FT	CONFLICT 166 166 C -> S (IN REF. 2).
FT	CONFLICT 183 183 MISSING (IN REF. 2).
SQ	SEQUENCE 410 AA; 43159 MW; 48FFA52D CRC32;
Query Match	3.3%; Score 118; DB 1; Length 410;
Best Local Similarity	27.4%; Pred. No. 3.36e-01; Length 410;
Matches	23; Conservative 22; Mismatches 35; Indels 3; Gaps 3;
Db	173 HHHHHHHHHHQHQALEGELLEHLHSPGIALGAMAGPDCAVSTPAHMHMTMPMHQA 233

QY	3	HHHHHHHHHHSSGGIDDDDKHMKKISSVYAI-ALFGTIAITANADLTASTTATLVEPPA	61
Db	233	ALSMAHAGL-P-SHMGCMSDVAD	255
Db	62	RITYREGAPITIMD-NGNIDNE	84
QY			
RESULT	12		
ID	BR11	BRARE	STANDARD;
AC	090436;	Q00433;	PRT;
DT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)	
01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)		
DT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)	
DT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)	
DE	BRAN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 1.1 (BRN-1.1) (FRAGMENT).		
BRN	1-1.		
OS	BRACHYONIO RERIO (ZEBRAFISH) (ZEBRA DANTO).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;		
OC	TELEOSTEI; EUTELEOSTEI; OSPIRORHYSI; CYPRINIFORMES; CYPRINOLEIDA;		
OC	CYPRINIDAE; RASBORINAE; DANIO.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	BRN-1.1.		
RA	SAMPATH K., STUART G.W.;		
RT	"Developmental expression of class III and IV POU domain genes in the zebrafish."		
RT	BLOCHM, BIOPHYS. RES. COMMON. 219:565-571(1996).		
CC	-!- FUNCTION: MAY PLAY A ROLE IN SPECIFYING TERMINALLY DIFFERENTIATED NEURONAL PHENOTYPES (BY SIMILARITY).		
CC	-!- SUBCELLULAR LOCATION: NUCLEAR.		
CC	-!- TISSUE SPECIFICITY: NERVOUS SYSTEM.		
CC	-!- DEVELOPMENTAL STAGE: EXPRESSED EARLY IN DEVELOPMENT AND IN THE ADULT BRAIN.		
CC	-!- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS TO CLASS-3 POU.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	DR	EMBL; AP000043; G1674128; -.	
CC	KW	HYDROLASE; MANGANESE.	
CC	SEQUENCE	733 AA; 86403 MW; 2654A136 CRC32;	
Query Match	3.2%	Score 114; DB 1; Length 733;	
Best Local Similarity	27.0%	Pred. No. 1.16e+00;	
Matches	33;	Conservative	
		Mismatches	45;
		Indels	10;
		Gaps	9;
Db	387	SRDPFKRIFGDTIKVNVSSDNEPNPKVNLKVNNSKLDIAYELVYLPQF-NKLEKIKLQD 445	
QY	162	SQDPFVRIGSKGKLA AGKY-TDAVT-VTV-SNQEMIRATEQNPORFIEDLEKVRVE 217	
DR	PFAM: PF00046; homeobox; 1.		
DR	EMBL: U43898; G1399384; -.		
DR	PROSITE: PS0007; HOMEBOX_1; 1.		
DR	PROSITE: PS0071; HOMEBOX_2; 1.		
DR	PROSITE: PS0035; POU_1; 1.		
DR	PROSITE: PS00465; POU_2; 1.		
DR	PFAM: PF00157; pou; 1.		
DR	HSSP: P14859; 1POU.		
KW	HOMEBOX; DNA-BINDING; TRANSCRIPTION REGULATION; NUCLEAR PROTEIN.		
FT	NON-TER	1	
FT	DOMAIN	228	299
FT	DNA-BIND	317	376
FT	DOMAIN	81	92
FT	DOMAIN	203	213
FT	SEQUENCE	406 AA;	43677 MW; DB96889B CRC32;
RESULT	13		
Best Local Similarity	56.5%	Pred. No. 9.11e-01;	
Matches	13;	Conservative	
		Mismatches	5;
		Indels	1;
		Gaps	1;
ID	SPOT-MCPN	STANDARD;	PRT;
ID	P75386;		
DT	01-NOV-1997	(REL. 35, CREATED)	
QY	1	MGHHHHHHHHSSGGIDDDKH 23	
RESULT	14		
ID	NIPLYEAST	STANDARD;	PRT;
AC	P33497;		
DT	01-OCT-1993	(REL. 27, CREATED)	
DT	01-OCT-1996	(REL. 34, LAST SEQUENCE UPDATE)	
DT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)	
DE	NUCLEAR TRANSPORT PROTEIN NIPI.		
GN	NIPL OR YM9309C OR YM9524.01C OR YM952.11C.		
OS	SACCHAROMYCES CEREFISIE (BAKER'S YEAST).		
OC	EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;		
OC	SACCHAROMYCETACEAE; SACCHAROMYCETES.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE; 93066237.		

QY	436	GSENRTGAGLNKNYSNKNDNELSHATASDKSRPLNDLVSKTQLSDTSRNS	495
RT		"Passive immunity to infection with <i>Yersinia</i> spp. mediated by anti-recombinant v antigen."	
RT		antigen. INNUN. 65:446-451(1997).	
RT		INFECT. IMMUN. 65:446-451(1997).	
RL		IMMUN. 65:446-451(1997).	
DR		EMBL: X96798; E23988; -.	
FT		NON-TER 35 325	
SQ		SEQUENCE 325 AA; 37260 MW; D6E88446 CRC32;	
RESULT	2		
ID	087495	PRELIMINARY; PRT; 324 AA.	
AC	087495;		
DT	01-NOV-1998 (TREMBREL. 08, LAST SEQUENCE UPDATE)		
DT	01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)		
DR		LCRV.	
OS		YERSINIA ENTEROCOLITICA.	
OC		BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIAE;	
KW		YERSINIA.	
SQ		SEQUENCE FROM N.A.	
RP		STRAIN=W22703;	
RA		TRIARTE M., LAMBERTON I., KERBOURCH C., CORNELIS G.R.;	
RT		COMPLETE SEQUENCE OF THE <i>Yersinia enterocolitica</i> PYY PLASMID.;	
RL		SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.	
DR		EMBL: AF080155; G3603358; -.	
OG		PLASMID PYY.	
KW		PLASMID.	
SEQUENCE	324 AA;	37296 MW; 7C9A652F CRC32;	
Query Match	60.9%	Score 2159; DB 2; Length 324;	
Best Local Similarity	95.4%	Pred. No. 0.00e+00;	
Matches	308;	Conservative 9; Mismatches 6; Indels 0; Gaps 0;	
Db	1	MIRAYEQNQFHFIGDLEKVRVDQIIGHGSVSVLEBLVQLVKDKKDISIKYDPKDSVEFA 60	
Qy	196	MIRAYEQNQFHFIGDLEKVRVDQIIGHGSVSVLEBLVQLVKDKKDISIKYDPKDSVEFA 255	
Db	1	MIRAYEQNQFHFIGDLEKVRVDQIIGHGSVSVLEBLVQLVKDKKDISIKYDPKDSVEFA 60	
Qy	256	MIRAYEQNQFHFIGDLEKVRVDQIIGHGSVSVLEBLVQLVKDKKDISIKYDPKDSVEFA 315	
Db	121	VMHFSLTADRIDDILKIVYDVMNMHHGDARSKLURELALTAELKKIVSYQAEINKYLN 180	
Qy	316	VMHFSLTADRIDDILKIVYDVMNMHHGDARSKLURELALTAELKKIVSYQAEINKHLS 375	
Db	181	SGTINIHDKSINLMKDNLYGTYDTEIFKSAEYKILEMSOTTIKEGETEKVLSIKFL 240	
Qy	376	SGTINIHDKSINLMKDNLYGTYDTEIFKSAEYKILEMSOTTIKEGETEKVLSIKFL 435	
Db	241	ESENKRTGAGLNKNYSNKNDNELSHATASDKSRPLNDLVSKTQLSDTSRNS 300	
Qy	436	GSENRTGAGLNKNYSNKNDNELSHATASDKSRPLNDLVSKTQLSDTSRNS 495	
Db	301	AIEALNRF+OKYDSVMQLDDT 323	
Qy	496	AIEALNRF+OKYDSVMQLDDT 518	
Db	61	DRVITDDIELKKILKLAFLPEDAIIKLGKHYDNLONGIKRKYKELESSPTQELRAMA 120	
Qy	256	NRVITDDIELKKILKLAFLPEDAIIKLGKHYDNLONGIKRKYKELESSPTQELRAMA 315	
Db	121	VMHFSLTADRIDDILKIVYDVMNMHHGDARSKLURELALTAELKKIVSYQAEINKHLS 180	
Qy	316	VMHFSLTADRIDDILKIVYDVMNMHHGDARSKLURELALTAELKKIVSYQAEINKHLS 375	
Db	181	SGTINIHDKSINLMKDNLYGTYDTEIFKSAEYKILEMSOTTIKEGETEKVLSIKFL 240	
Qy	376	SGTINIHDKSINLMKDNLYGTYDTEIFKSAEYKILEMSOTTIKEGETEKVLSIKFL 435	
Db	241	ESENKRTGAGLNKNYSNKNDNELSHATASDKSRPLNDLVSKTQLSDTSRNS 300	
Qy	436	GSENRTGAGLNKNYSNKNDNELSHATASDKSRPLNDLVSKTQLSDTSRNS 495	
Db	301	AIEALNRF+OKYDSVMQLDDT 323	
Qy	496	AIEALNRF+OKYDSVMQLDDT 518	
RESULT	4		
ID	056882	PRELIMINARY; PRT; 324 AA.	
AC	056882;		
DT	01-NOV-1996 (TREMBREL. 01, CREATED)		
DT	01-NOV-1996 (TREMBREL. 01, LAST SEQUENCE UPDATE)		
DT	01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)		
DR		V ANTIGEN	
OS		YERSINIA ENTEROCOLITICA.	
OC		BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIAE;	
RN		YERSINIA.	
RP		SEQUENCE FROM N.A.	
RC		STRAIN=Y-96-P;	
RX		MEDLINE; 97163308.	
ROGENKAMP A., GEIGER A.M., LEITRITZ L., KESSLER A., HEESMANN J.;		ROGENKAMP A., GEIGER A.M., LEITRITZ L., KESSLER A., HEESMANN J.;	
RT		"Passive immunity to infection with <i>Yersinia</i> spp. mediated by anti-recombinant v antigen is dependent on polymorphism of v antigen."	
RT		INFECT. IMMUN. 65:446-451(1997).	
RL		EMBL: X96801; E23998; -.	
DR		SEQUENCE 324 AA; 37162 MW; 56842DA CRC32;	
RESULT	3		
ID	056880	PRELIMINARY; PRT; 325 AA.	
AC	056880;		
DT	01-NOV-1996 (TREMBREL. 01, CREATED)		
DT	01-NOV-1996 (TREMBREL. 01, LAST SEQUENCE UPDATE)		
DT	01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)		
DE		V ANTIGEN (FRAGMENT).	
OS		YERSINIA ENTEROCOLITICA.	
OC		BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIAE;	
OC		YERSINIA.	
RN		YERSINIA.	
RP		SEQUENCE FROM N.A.	
RC		STRAIN=W801;	
RX		MEDLINE; 97163308.	
ROGENKAMP A., GEIGER A.M., LEITRITZ L., KESSLER A., HEESMANN J.;		ROGENKAMP A., GEIGER A.M., LEITRITZ L., KESSLER A., HEESMANN J.;	
RT		"Passive immunity to infection with <i>Yersinia</i> spp. mediated by anti-recombinant v antigen is dependent on polymorphism of v antigen."	
RT		INFECT. IMMUN. 65:446-451(1997).	
RL		EMBL: X96801; E23998; -.	
DR		SEQUENCE 324 AA; 37162 MW; 56842DA CRC32;	
Query Match	60.0%	Score 2128; DB 2; Length 324;	
Best Local Similarity	93.8%	Pred. No. 0.00e+00;	
Matches	303;	Conservative 12; Mismatches 8; Indels 0; Gaps 0;	
Db	1	MIRAYEQNQFHFIGDLEKVRVDQIIGHGSVSVLEBLVQLVQDKKDISIKYDPKDSVEFA 60	
Qy	196	MIRAYEQNQFHFIGDLEKVRVDQIIGHGSVSVLEBLVQLVQDKKDISIKYDPKDSVEFA 255	
Db	121	VMHFSLTADRIDDILKIVYDVMNMHHGDARSKLURELALTAELKKIVSYQAEINKHLS 180	

Db	61	ERVITDIELLKKILAYFLPEDAIIKGGHYDNLQNGIKRVEFLESSPNTQWELRagma	120	RESULT 9	PRELIMINARY;	PRT; 294 AA.
Qy	:	: : : : : :	120	ID 030527;	PRELIMINARY;	PRT; 294 AA.
Db	256	NRVITDIELLKKILAYFLPEDAIIKGGHYDNLQNGIKRVEFLESSPNTQWELRagma	315	AC 030527;	PRELIMINARY;	PRT; 294 AA.
Qy	121	VMHFSLTADRIDDLKVIVDSMNMHGDKRSKREELAELTAELKIVSIVQAEINKHSS	180	DT 01-NOV-1998 (TREMBLREL. 05, CREATED)	PRELIMINARY;	PRT; 294 AA.
Db	316	VMHFSLTADRIDDLKVIVDSMNMHGDKRSKREELAELTAELKIVSIVQAEINKHSS	375	DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)	PRELIMINARY;	PRT; 294 AA.
Qy	181	SGTINTHEKSNLMDKNLYGTDDELFKASAELYKILKMPOTIKDDELHEVGVGAEK	240	DE PCRV.	PRELIMINARY;	PRT; 294 AA.
Db	376	SGTINTHDKSNLMDKNLYGTDDELFKASAELYKILKMPOTIKDDELHEVGVGAEK	375	GN PCRV.	PRELIMINARY;	PRT; 294 AA.
Qy	241	QIVSIKNFLESENKRKGALGNLKDSYNKDNNEELSHFATACSDKSRPLNDLVSQTTQ	300	OS PSEUDOMONAS AERUGINOSA.	PRELIMINARY;	PRT; 294 AA.
Qy	427	KIVSIKDFLGSEBNKRKGALGNLKDSYNKDNNEELSHFATCSDKSRPLNDLVSQTTQ	486	OC PSEUDOMONAS.	PRELIMINARY;	PRT; 294 AA.
Db	301	SDITSRNSATEALNRFIQKDSVMQRLLDT	332	OC PSEUDOMONAS.	PRELIMINARY;	PRT; 294 AA.
Qy	487	SDITSRNSATEALNRFIQKDSVMQRLLDT	518	OC PSEUDOMONAS.	PRELIMINARY;	PRT; 294 AA.
SO				RN [1]	SEQUENCE FROM N A.	
RESULT 8				RP	SEQUENCE FROM N A.	
ID 056895		PRELIMINARY;	PRT; 334 AA.	RC STRAIN=388;	SEQUENCE FROM N A.	
AC Q56895;				RX MEDLINE; 9803717.	SEQUENCE FROM N A.	
DT 01-NOV-1995 (TREMBLREL. 01, CREATED)				RA YAHR T. L., MENDZ-MUELLER L. M., FRISSE M. B., FRANK D. W.,	SEQUENCE FROM N A.	
DT 01-NOV-1995 (TREMBLREL. 01, LAST SEQUENCE UPDATE)				RT "Identification of type III secreted products of the Pseudomonas aeruginosa exoenzyme S regulon.";	SEQUENCE FROM N A.	
DE V ANTIGEN (FRAGMENT)				RT J. BACTERIOL. 179:7165-7168(1997).	SEQUENCE FROM N A.	
OS VERSINTIA ENTEROCOLITICA.				RL EMBL; AF010149; G2459968; -;	SEQUENCE FROM N A.	
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;				DR EMBL; AF010149; G2459968; -;	SEQUENCE FROM N A.	
RN [1]				SO SEQUENCE 294 AA; 32283 MW; OFAB2082 CRC32;	SEQUENCE FROM N A.	
RP SEQUENCE FROM N A.						
RC STRAIN=NCTC;						
RX MEDLINE; 97162308.						
RA ROGGENKA A., GEIGER A.M., LEITRITZ L., KESSLER A., HESEMMANN J.;						
RT "Passive immunity to infection with <i>Yersinia</i> spp. mediated by anti-recombinant v antigen is dependent on polymorphism of v antigen."						
RT INFECT. IMMUN. 65:446-451(1997).						
RL EMBL; X96797; B239983; -.						
DR NON_TER 334						
FT 334 AA; 38227 MW; F23FDFD3 CRC32;						
SO SEQUENCE 334 AA; 38227 MW; F23FDFD3 CRC32;						
Query Match 58.5%; Score 2074; DB 2; Length 334;						
Best Local Similarity 92.8%; Pred. No. 0; 0.0e+00;						
Matches 308; Conservative 11; Mismatches 4; Indels 9; Gaps 3;						
Db 1 MIRAYFQNPOHFTEDLEKVRVQDQTLGHGSSYLEVOLVKDKPDKPQSEVFA	60	RESULT 10	18.4%; Score 653; DB 2; Length 294;			
Qy 196 MIRAYFQNPOHFTEDLEKVRVQDQTLGHGSSYLEVOLVKDKPDKPQSEVFA	255	ID Q16256	PRELIMINARY;	PRT; 168 AA.		
Db 61 ERVITDIELLKKILAYFLPEDAIIKGGHYDNLQNGIKRVEFLESSPNTQWELRagma	120	AC 016256;	PRELIMINARY;	PRT; 168 AA.		
Qy 256 NRVITDIELLKKILAYFLPEDAIIKGGHYDNLQNGIKRVEFLESSPNTQWELRagma	315	DT 01-NOV-1995 (TREMBLREL. 01, CREATED)	PRELIMINARY;	PRT; 168 AA.		
Db 121 VMHFSLTADRIDDLKVIVDSMNMHGDKRSKREELAELTAELKIVSIVQAEINKHSS	180	DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)	PRELIMINARY;	PRT; 168 AA.		
Qy 316 VMHFSLTADRIDDLKVIVDSMNMHGDKRSKREELAELTAELKIVSIVQAEINKHSS	375	DE WT1=WILMS' TUMOR SUPPRESSOR PROTEIN.	PRELIMINARY;	PRT; 168 AA.		
Db 181 SGTINTHEKSNLMDKNLYGTDDELFKASAELYKILKMPOTIKDDELHEVGVGAEK	240	GN WT1.	PRELIMINARY;	PRT; 168 AA.		
Qy 376 SGTINTHDKSNLMDKNLYGTDDELFKASAELYKILKMPOTIKDDELHEVGVGAEK	426	OS HOMO SAPIENS (HUMAN).	PRELIMINARY;	PRT; 168 AA.		
Db 241 QIVSIKNFLESENKRKGALGNLKDSYNKDNNEELSHFATACSDKSRPLNDLVSQTTQ	300	OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;	PRELIMINARY;	PRT; 168 AA.		
Qy 427 KIVSIKDFLGSEBNKRKGALGNLKDSYNKDNNEELSHFATCSDKSRPLNDLVSQTTQ	486	OC CATARRHINI; HOMINIDAE; HOMO.	PRELIMINARY;	PRT; 168 AA.		
Db 301 SDITSRNSATEALNRFIQKDSVMQRLLDT	332	RN [1]	SEQUENCE FROM N A.	PRELIMINARY;	PRT; 168 AA.	
Qy 487 SDITSRNSATEALNRFIQKDSVMQRLLDT	518	RP SEQUENCE FROM N A.	SEQUENCE FROM N A.	PRELIMINARY;	PRT; 168 AA.	
Query Match 4.7%; Score 168; DB 4; Length 168;						
Best Local Similarity 66.7%; Pred. No. 1.19e-05;						
Matches 20; Conservative 7; Mismatches 1; Indels 2; Gaps 1;						
Db 1 MGHNNHHHHHHSSGGHIEG--RHMRVPGV 28						

Search completed: Sat Nov 27 15:36:59 1999
Job time : 101 secs.

PT	Yersinia pestis V antigen and F1 antigen or their protective epitopic parts - useful in vaccine for protection against plague
PT	Disclosure: Page 25-28; 98pp; English.
CC	Yersinia pestis V antigen (W01040) is capable of evoking protective immune responses in animals. A combined vaccine of V and F1 antigens (see also W01042) can at least match the protection afforded by live attenuated EV76 vaccine without any of the hazards that have kept the EV vaccine from general use. The V antigen is produced using the lcrV gene (see also T38242) obt. from Y. pestis by PCR amplification. It can also be prep. as a fusion with F1 antigen (see also W01044-45) and expressed by attenuated AroA or C Salmonella typhi as a live vaccine for long-term protection against plague. Expression by gut-colonising bacterial transformants produces a protective response against Y. pestis.
SQ	Sequence 329 AA:
Query Match	63.2%; Score 2242; DB 19; Length 329;
Best Local Similarity	99.4%; Pred. No. 2.16e-156;
Matches	326; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Db	3 ef_irayeqnpqhfiedlekvrveqtlghgssvleelvqlvkdnidisikydpksev 61
Qy	194 EFMRAYECPNPQHIEDLEKVRVEQTLGHGSSVLEELVQLVKDNIDISKYDPKSEV 253
Db	62 fanrvitddielkkilayflpedailkgghydnqglngqikvkefessontqwlraf 121
Qy	254 FANRVITDIELKKILAYFLPDTIKGGHDNQLONGIKRVEFLESSPNTQWLRAF 313
Db	122 mavmhfsitadrrddilkvivdsmnhgdaaskrlrealetaelkiyvqaehnhl 181
Qy	314 MAVMHFSITADRRDDILKIVIVDSMNHGDAKSRLREALETAELKIYVQAENHL 373
Db	182 sssgtinidksinlmdknlyyytdeefkasaeykilekmpqtqydgsekkivskd 241
Qy	374 SSSGTINIDKSINLMDKNLYYYTDEEFKASAAYKILEKMPQTQYDGSEKKIVSKD 433
Db	242 flgsenkrtgalgnlknsysynkdnelshtatcsksrplndvsgktqldtsrf 301
Qy	434 FLSENKRITGALGNLKNSYSYNKNDNELSHATCSDKSRSRPLNDVSQKTTQLDTSRF 493
Db	302 nsiaealnrfiqkydsvmgqrlddtsk 329
Qy	494 NSIAEALNRFIQKYDSDVMQLDDTSK 521
RESULT	5
ID	W01041 standard; Protein; 329 AA.
AC	R79961; 18-APR-1996 (first entry)
DT	Partial lcrV (V antigen) of Y. pestis.
KW	lcrV; V antigen; virulence; plague; vaccine; epitope.
OS	Yersinia pestis.
PN	W0924475-A1.
PD	14-SEP-1995.
PF	06-MAR-1995; G00481.
PR	08-MAR-1994; GB-004577.
PA	(MINA) UK SEC FOR DEFENCE.
PA	Y. pestis V antigen (W01041) is capable of evoking protective immune responses in animals. A combined vaccine of V and F1 antigens (see also W01042) can at least match the protection afforded by live attenuated EV76 vaccine without any of the hazards that have kept the EV vaccine from general use. The V antigen is produced using the lcrV gene (see also T38243) obt. from Y. pestis by PCR amplification. It can also be prep. as a fusion with F1 antigen (see also W01044-45) and expressed by attenuated AroA or C Salmonella typhi and gut-colonising bacteria for protection against plague.
SQ	Sequence 329 AA:
Query Match	63.1%; Score 2236; DB 19; Length 329;
Best Local Similarity	99.7%; Pred. No. 6.15e-156;
Matches	324; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db	5 irayeqnpqhfiedlekvrveqtlghgssvleelvqlvkdnidisikydpksevfan 64

QY	197	IRAYEONPQHFIELDKVRVQEQLTGHSVYLEELVOLVKRKNIDISIKYDPRKSEVEN	256	Db	245	sekntgaglnkakasysynphanneshfttcsksrpnlndsgtqrlsldtsrfsa	304
Db	65	rvtdielkkklayflpedailkgghydnqlqngikrykfessptqwerafmav	124	QY	437	SENKRIGALNKLNSYSYNKDNNELESHATTCSDKSRPLNDVSQTKTOLSDITSRFNSA	496
QY	257	RVTDIIEELKKKLLAYFLPEDTLLKGHHYDNLQNGIKRYKEFLESSPTQWEARFMAV	316	Db	305	iealnrfiqydswnqrldtsk	329
Db	125	mhfstdriddikkvivsnnhingdarkrlreelaetaelklysvqaenihlss	184	QY	317	MHFSLTADRIDDDILKIVPSMNHHGARDASKRLEELAELTAELKLYSVI	376
QY	377	GTINHDKSINLMDKNULYGVYDEIFKASAEYKILEKMPPTIGDQSGTKEVREINHLSS	376	RESULT	7	standard; Protein: 170 AA.	
Db	185	gtinlhdksnlmknlygtdeefkasaykilekmpptigdsgtkevresikdfg	244	ID	W01043	standard; Protein: 170 AA.	
QY	377	GTINHDKSINLMDKNULYGVYDEIFKASAEYKILEKMPPTIGDQSGTKEVREINHLSS	376	AC	W01043;		
Db	245	sekntgaglnkakasysynphanneshfttcsksrpnlndsgtqrlsldtsrfsa	304	DT	28-DEC-1996	(first entry)	
QY	437	SENKRIGALNKLNSYSYNKDNNELESHATTCSDKSRPLNDVSQTKTOLSDITSRFNSA	496	DE	Y. pestis F1 antigen (including signal peptide).		
Db	437	SENKRIGALNKLNSYSYNKDNNELESHATTCSDKSRPLNDVSQTKTOLSDITSRFNSA	496	KW	Plague; vaccine; genetic immunisation; F1 antigen; cafl;		
QY	437	SENKRIGALNKLNSYSYNKDNNELESHATTCSDKSRPLNDVSQTKTOLSDITSRFNSA	496	KW	V antigen.		
Db	305	iealnrfiqydswnqrldtsk	329	OS	versinia pestis strain GB		
QY	497	IEALNRFIOKYDSVMORLDDTSK	521	FT	Key	Location/Qualifiers	
RESULT	6			FT	peptide	1..21	
ID	R79962	standard; Protein: 329 AA.		FT	label=	Sig-peptide	
AC	R79962			PN	W09620551-Al.		
DT	18-APR-1996	(first entry)		PD	19-SEP-1996.		
DE	Partial LcrV (V antigen) of Y. pestis.			PR	13-MAR-1996; GO0571		
KW	LcrV; V antigen; virulence; plague; vaccine; epitope.			PR	13-MAR-1995; GO-005059		
OS	Yersinia pestis.			PR	15-SEP-1995; GO-018946.		
PD	W09524751-Al.			PR	05-DEC-1995; GO-024825.		
PP	14-SEP-1995.			PA	(MINA) UK SEC FOR DEFENCE.		
PR	06-MAR-1995; GO0481			PI	Bennett AM, Leary SEC, Oyston PCF, Titball RW, Williamson ED;		
PR	08-MAR-1995; GB-004577.			DR	WPI: 96-33824/43.		
PA	(MINA) UK SEC FOR DEFENCE.			N-PSDB	WPI: 96-33824/43.		
PI	Leary SEC, Titball RW, Williamson ED, Leary SE;			PT	Yersinia pestis V antigen and F1 antigen or their protective epitopic parts - useful in vaccine for protection against plague		
DR	WPI: 95-320268/42.			PS	Example 2; Page 61-62; 98pp; English.		
DR	WPI: 95-320268/42.			CC	The F1 antigen (W01043), including the signal peptide, of Yersinia pestis was produced from a DNA sequence (T38248) obtained by PCR amplification (see also T38257-58) of Y. pestis DNA. Expression of the F1 antigen (see also W01042), by gut-colonising organisms in the form of live vaccines (see also W01042), can be used to protect an animal, including humans, against plague.		
PT	Recombinant DNA expressing Yersinia pestis V antigen - useful in oral or parenteral vaccines for protection against plague			CC	CC		
PT	Claim 6; Page 15-16; 25pp; English.			CC	CC		
CC	R79951-62 are encoded by T04222-23 (resp.), DNA sequences (lcrV) encoding all or a protective epitopic part of the mature V protein of Yersinia pestis. The protein was expressed as a fusion protein with maltose binding protein or glutathione-S-transferase in 3 different plasmid vectors. Y. pestis is the highly virulent causative organism of plague in a wide range of animals, including man. The V antigen (lcrV) is an unstable 37.3 kDa monomeric peptide encoded on the ca. 70 kb lcr plasmid. The V antigen is postulated to act as a virulence antigen, and transformed microorganisms containing recombinant DNA encoding a V antigen protein/peptide are useful in vaccines to protect against plague.			SQ	Sequence		
CC	transformed microorganisms containing recombinant DNA encoding a V antigen protein/peptide are useful in vaccines to protect against plague.			Query	Match	Best Local Similarity 31.0%; Score 1100; DB 19; Length 170; Best Local Similarity 100.0%; Score 1100; DB 19; Length 170; Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
CC	329 AA;			Matches			
Matches	323; Conservative 2; Mismatches 0; Indels 0; Gaps 0;			Db	1	mkkissviaalftiataanaditasttattatativeparitlykegaptintangnptd	60
Db	6	mkkissviaalftiataanaditasttattatativeparitlykegaptintangnptd	60	QY	24	MKKISSVIAALFGTTATANADATRSTRATLVEPARTLYKEGAPTTIMGNIDT	83
Db	61	elvygtlqyktgttstsvnftdaagpnyiftsgqgnhfttkvqgkrsdfis	120	QY	84	ELVGTlqyktgttstsvnftdaagpnyiftsgqgnhfttkvqgkrsdfis	143
Db	121	pkvngnlgdvvlatgscdfifrsigskggklaagkttdavtvnsq	170	QY	144	PKVNGNlgdvvlatgscdfifrsigskggklaagkttdavtvnsq	193
QY	197	IRAYEONPQHFIELDKVRVQEQLTGHSVYLEELVOLVKRKNIDISIKYDPRKSEVEN	256	RESULT	8		
QY	197	IRAYEONPQHFIELDKVRVQEQLTGHSVYLEELVOLVKRKNIDISIKYDPRKSEVEN	256	ID	R76528	standard; Protein: 170 AA.	
Db	65	rvtdielkkklayflpedailkgghydnqlqngikrykfessptqwerafmav	124	AC	R76528;		
Db	257	RVTDIIEELKKKLLAYFLPEDTLLKGHHYDNLQNGIKRYKEFLESSPTQWEARFMAV	316	DT	17-DEC-1995	(first entry)	
Db	125	mhfstdriddikkvivsnnhingdarkrlreelaetaelklysvqaenihlss	184	DE	Yersinia Pestis cafl (F1) antigen.		
QY	317	MHFSLTADRIDDDILKIVPSMNHHGARDASKRLEELAELTAELKLYSVI	376	KW	Vaccine; antigen; Salmonella typhimurium; Salmonella typhi; bubonic; plague; pneumonic plague.		
QY	317	MHFSLTADRIDDDILKIVPSMNHHGARDASKRLEELAELTAELKLYSVI	376	OS	Yersinia pestis.		
QY	317	MHFSLTADRIDDDILKIVPSMNHHGARDASKRLEELAELTAELKLYSVI	376	PN	W09518231-Al.		
Db	185	gtinlhdksnlmknlygtdeefkasaykilekmpattiqdgsekkivsikdfg	244	PP	06-JUL-1995.		
Db	377	GTINHDKSINLMDKNULYGVYDEIFKASAEYKILEKMPPTIGDQSGTKEVREINHLSS	376	PR	23-DEC-1994; GO2818.		
QY	377	GTINHDKSINLMDKNULYGVYDEIFKASAEYKILEKMPPTIGDQSGTKEVREINHLSS	376	PR	24-DEC-1993; GB-026425.		
QY	377	GTINHDKSINLMDKNULYGVYDEIFKASAEYKILEKMPPTIGDQSGTKEVREINHLSS	376	PA	(MINA) UK SEC FOR DEFENCE.		
QY	377	GTINHDKSINLMDKNULYGVYDEIFKASAEYKILEKMPPTIGDQSGTKEVREINHLSS	376	PI	Howells A, Leary SEC, Oyston PCF, Titball RW, Williamson ED;		
DR	~2~			DR	WPI: 95-246396/32.		

DR N-PSDB; 092819.
 PT DNA constructs capable of transforming microorganisms - which can be used as live or attenuated vaccines which induce an immune response, against *Yersinia pestis*, at mucosal surfaces.
 PT Disclosure; page 20; 27pp; English.
 CC The sequence represents the *Y. pestis* cafl (F1) antigen expressed from plasmid pF08Bf. The DNA construct can be used to transform human or animal gut colonizing microorganisms, specifically attenuated *Salmonella typhimurium* or *Salmonella typhi*. The transformed microorganisms can be used as live/attenuated vaccines which induce immune responses at mucosal surfaces. The vaccines provide protection against infection with *Y. pestis*, and are parenterally and orally active vaccines offering protection against bubonic and pneumonic plague.
 CC Sequence 170 AA;

Query Match 31.0%; Score 1100; DB 14; Length 170;
 Best Local Similarity 100.0%; Pred. No. 3.31e-70;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PR 04-DEC-1996; US 767115.
 PT 04-DEC-1997; U22617.
 ID W59782 standard; Protein; 170 AA.
 AC W59782;
 QY 24 MKKISSVIALFCTIATANAADITASTTATIVEPARITLYKEGAPITIMGNIDT 83
 Db 61 elvgltlqgkgttstsvnfdaaagpmyltfsqgnhafftkvigkarsrdfs 120
 QY 84 ELLVGTLTQGKGTTSVNFDAAGPMLFTSQDGNHOFPTKVKIGKDSRDFDIS 143
 Db 121 pkvngenvlgddvvlatgsqffvrsigskgklaagkytdavtvtsq 170
 QY 144 PKVNGENLVGDDVVLATGSQDFFVRSIGSKGGKLAAGKYTDATVTVSNG 193
 RESULT 9
 ID W59783 standard; Protein; 170 AA.
 AC W59783;
 DT 26-OCT-1998 (first entry)
 DE Amino acid sequence of F1 antigen npF1sec510.
 KW F1 antigen; plasmid; vaccine; plague; ds.
 OS Yersinia pestis.
 FH Key Location/Qualifiers
 CC 17.5.32
 FT /*tag= a
 FT /product= "F1 antigen"
 PN W09824912-A2.
 PD 11-JUN-1998.
 PR 04-DEC-1997; U22617.
 PR 04-DEC-1996; US-767115.
 PA (HEK-) HESKA CORP.
 PI Haanes EJ, Osorio JE, Thomas RE;
 DR WPI; 98-33331/29.
 N-PSDB; v41596.
 PT Protection of animals against plague - using nucleic acid encoding protection of animals against plague - using nucleic acid encoding antigen from *Yersinia*, *Pasteurella* and *Francisella* spp.
 PT Disclosure: Pages 53-54; 75pp; English.
 CC This is the amino acid sequence of a *Yersinia pestis* F1 antigen, used in the method of the invention. Plasmid and host cells are used to produce recombinant antigens, especially *Yersinia pestis* antigens. The recombinant antigens can be used in vaccines that are capable of protecting an animal from contracting plague.
 CC Sequence 170 AA;

Query Match 31.0%; Score 1100; DB 34; Length 170;
 Best Local Similarity 100.0%; Pred. No. 3.31e-70;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PR 04-DEC-1997; U22617.
 ID W59788 standard; Protein; 149 AA.
 AC W59788;
 DT 26-OCT-1998 (first entry)
 DE Nucleotide sequence of F1 antigen npF1mat149.
 KW F1 antigen; plasmid; vaccine; plague.
 OS Yersinia pestis.
 PN W09824912-A2.
 PD 11-JUN-1998.
 PR 04-DEC-1997; U22617.
 PR 04-DEC-1996; US-767115.
 PA (HEK-) HESKA CORP.
 PI Haanes EJ, Osorio JE, Thomas RE;
 DR WPI; 98-33331/29.
 N-PSDB; v41609.
 PT Protection of animals against plague - using nucleic acid encoding antigen from *Yersinia*, *Pasteurella* and *Francisella* spp.
 CC This is the amino acid sequence of a *Yersinia pestis* F1 antigen, used in the method of the invention. Plasmid and host cells are used to produce recombinant antigens, especially *Yersinia pestis* antigens. The recombinant antigens can be used in vaccines that are capable of protecting an animal from contracting plague.
 CC Sequence 149 AA;

Query Match 31.0%; Score 1100; DB 34; Length 170;
 Best Local Similarity 100.0%; Pred. No. 3.31e-70;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PR 04-DEC-1997; U22617.
 ID W59782 standard; Protein; 170 AA.
 AC W59782;
 DT 26-OCT-1998 (first entry)
 DE Amino acid sequence of F1 antigen npF1sec170.
 KW F1 antigen; plasmid; vaccine; plague.
 OS Yersinia pestis.
 PN W09824912-A2.
 PD 11-JUN-1998.
 PR 04-DEC-1997; U22617.
 ID W59782;
 QY 144 PKVNGENLVGDDVVLATGSQDFFVRSIGSKGGKLAAGKYTDATVTVSNG 193
 RESULT 10
 ID W59782 standard; Protein; 170 AA.
 AC W59782;
 DT 26-OCT-1998 (first entry)
 DE Amino acid sequence of F1 antigen npF1sec170.
 KW F1 antigen; plasmid; vaccine; plague.
 OS Yersinia pestis.
 PN W09824912-A2.
 PD 11-JUN-1998.
 PR 04-DEC-1997; U22617.
 ID W59782;
 QY 144 PKVNGENLVGDDVVLATGSQDFFVRSIGSKGGKLAAGKYTDATVTVSNG 193
 RESULT 11
 ID W59788 standard; Protein; 149 AA.
 AC W59788;
 DT 26-OCT-1998 (first entry)
 DE Nucleotide sequence of F1 antigen npF1mat149.
 KW F1 antigen; plasmid; vaccine; plague.
 OS Yersinia pestis.
 PN W09824912-A2.
 PD 11-JUN-1998.
 PR 04-DEC-1997; U22617.
 PR 04-DEC-1996; US-767115.
 PA (HEK-) HESKA CORP.
 PI Haanes EJ, Osorio JE, Thomas RE;
 DR WPI; 98-33331/29.
 N-PSDB; v41609.
 PT Protection of animals against plague - using nucleic acid encoding antigen from *Yersinia*, *Pasteurella* and *Francisella* spp.
 CC This is the amino acid sequence of a *Yersinia pestis* F1 antigen, used in the method of the invention. Plasmid and host cells are used to produce recombinant antigens, especially *Yersinia pestis* antigens. The recombinant antigens can be used in vaccines that are capable of protecting an animal from contracting plague.
 CC Sequence 149 AA;

Query Match	27.4%	Score 971; DB 34; Length 149;	PA (MINA) UK SEC FOR DEFENCE.
Best Local Similarity	100.0%	Pred. No. 1.42e-60;	PI Bennett AM, Lairy SEC, Oyston PCF, Titball RW, Williamson ED;
Matches	149; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	DR WPI; 96-433824/43.
Db	1 adltasttatativeparititykegapitindngidtelvgltlgyktgtstsv	60	PR N-PSDB; T8244.
Qy	45 ADLTASTTATATIVEPARITITYKEGAPITINDNGIDTELVLGTLGGYKTGTSTSV	104	PR Yersinia pestis V antigen and F1 antigen or their protective epitopic parts - useful in vaccine for protection against plague disclosure; Page 43-45; 98PP; English.
Db	61 nftdaagdpmylftsqdgnhafkttkvigkdsrdspkvngevlvgdawvlatgsqd	120	PS Yersinia pestis F1 antigen (W0142) is capable of evoking protective immune responses in animals. A combined vaccine of F1 and V antigens (see also W01041-41) can at least match the protection afforded by live attenuated EV76 vaccine without any of the hazards that have kept the EV vaccine from general use. The F1 antigen is produced using the cat1 gene (see also T3824) optd. from Y. pestis by PCR amplification. It can also be prep. as a fusion with V antigen (see also W0104-45) and expressed by attenuated Aroa or C. Salmonella typhi as a live vaccine for long-term protection
Qy	105 NFTDAAGDPMLFTSQDGNHAFKTTKVIGKDSRDSPKVNGENLVGDDVLATGSQD	164	CC produced using the cat1 gene (see also T3824) optd. from Y. pestis by PCR amplification. It can also be prep. as a fusion with V antigen (see also W0104-45) and expressed by attenuated Aroa or C. Salmonella typhi as a live vaccine for long-term protection
Db	121 ffvrsigskgklaakydavtvtsnq	149	CC against plague. Expression by gut-colonising bacterial transformants produces a protective response against Y. pestis.
Qy	165 FFVRSIGSKGKLAAGKYTDATVTVSNO	193	CC Sequence 151 AA;
RESULT	12		SQ
ID	W59787	standard; Protein; 150 AA.	
AC	W59787;		
DT	26-OCT-1998	(first entry)	
DE	Amino acid sequence of F1 antigen pYpFImat150.		
KW	F1 antigen; Plasmid; vaccine; Plague.		
OS	Yersinia pestis.		
PN	W0924912-42.		
PD	11-JUN-1998		
PF	04-DEC-1997; U22617		
PR	04-DEC-1996; US-767115.		
PA	(HESK-) HESEA CORP.		
PT	Haanes EJ, Osorio JE, Thomas RE;		
DR	WPI; 98-33312/29.		
DR	N-PSDB; V41600.		
PT	protection of animals against plague - using nucleic acid encoding antigen from Yersinia, Pasteurella and Francisella spp.		
PS	Claim 10; Page 60; 75PP; English.		
CC	This is the amino acid sequence of a Yersinia pestis F1 antigen, used in the method of the invention. Plasmid and host cells are used to produce recombinant antigens, especially Yersinia pestis antigens.		
CC	The recombinant antigens can be used in vaccines that are capable of protecting an animal from contracting plague.		
Sequence	150 AA;		
Query Match	27.4%	Score 971; DB 34; Length 150;	
Best Local Similarity	100.0%	Pred. No. 1.42e-60;	
Matches	149; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Db	2 adltasttatativeparititykegapitindngidtelvgltlgyktgtstsv	61	
Qy	45 ADLTASTTATATIVEPARITITYKEGAPITINDNGIDTELVLGTLGGYKTGTSTSV	104	
Db	62 nftdaagdpmylftsqdgnhafkttkvigkdsrdspkvngevlvgdawvlatgsqd	121	
Qy	105 NFTDAAGDPMLFTSQDGNHAFKTTKVIGKDSRDSPKVNGENLVGDDVLATGSQD	164	
Db	122 ffvrsigskgklaakydavtvtsnq	150	
Qy	165 FFVRSIGSKGKLAAGKYTDATVTVSNO	193	
RESULT	14		
ID	R76525	standard; Protein; 151 AA.	
AC	R76526;		
DT	17-DEC-1995	(first entry)	
DE	Yersinia pestis caf1 (F1) antigen.		
KW	Vaccine; antigen; Salmonella typhimurium; Salmonella typhi; bubonic plague; pneumonic plague.		
OS	Yersinia pestis.		
PN	W09518231-A1.		
PD	06-JUL-1995.		
PF	23-DEC-1994; G02818		
PR	24-DEC-1993; GB-026425.		
PA	(MINA) UK SEC FOR DEFENCE.		
PI	Howells A, Lairy SEC, Oyston PCF, Titball RW, Williamson ED;		
DR	WPI; 95-24639632.		
DR	N-PSDB; Q02817.		
PT	DNA constructs capable of transforming microorganisms - which can be used as live or attenuated vaccines which induce an immune response, PT against Yersinia pestis, at mucosal surfaces.		
PS	Disclosure; Page 16; 27PP; English.		
CC	The sequence represents the Y. pestis caf1 (F1) antigen expressed from plasmid pYca12. The DNA construct can be used to transform human or animal gut colonizing microorganisms, specifically attenuated Salmonella typhimurium or Salmonella typhi. The transformed microorganisms can be used as live/attenuated vaccines which induce immune responses at mucosal surfaces. The vaccines provide protection against infection with Y. pestis, and are parenterally and orally active vaccines offering protection		
CC	against bubonic and pneumonic plague.		
SQ	Sequence 151 AA;		
Query Match	27.3%	Score 968; DB 14; Length 151;	
Best Local Similarity	98.0%	Pred. No. 2.38e-60;	
Matches	148; Conservative	3; Mismatches 0; Indels 0; Gaps 0;	
Db	1 ssadltasttatativeparititykegapitindngidtelvgltlgyktgtst	60	

QY	43	NADLDTASTTATATLVEPARITYKEGAPITIMDNGNIDTTELVLGTLTGYKGTTST	102
Db	61	svnftdaagpmlylttsqsdnnhgfkttkvkgkdsrdflspkvngnlvgddvlatgs	120
Oy	103	SVNFDTDAAGPMLYLTTSQSDNNHGFKTTKVKGKDSRDFDISPKVNGNLVGDDVLATGS	162
Db	121	qdfvrsigsgklaagkytdavtvnsq 151	
Oy	163	qdfvrsigsgklaagkytdavtvnsq 193	
	RESULT	15	
ID	R76527	standard; Protein: 151 AA.	
AC	R76527;		
DR	17-DEC-1995	(first entry)	
DE	Versinia pestis caf1 (F1) antigen.		
KW	Vaccine; antigen; <i>Salmonella typhimurium</i> ; <i>Salmonella typhi</i> ; bubonic plague; pneumonic plague.		
OS	Versinia pestis.		
PN	W0958231-A1		
PD	06-JUL-1995.		
PF	23-DEC-1994; GB-03818.		
PR	24-DEC-1993; GB-026425.		
PA	(MINA) UK SEC FOR DEFENCE.		
PI	Howells A, Leahy SEC, Oyston PCF, Titball RW, Williamson ED;		
DR	WPI: 95-243396732.		
NP-PSDB:	Q9818.		
PT	DNA constructs capable of transforming microorganisms - which can be used as live or attenuated vaccines which induce an immune response, against <i>Versinia pestis</i> , at mucosal surfaces.		
PT	Disclosure; Page 18; 27pp; English.		
PS	The sequence represents the <i>V. pestis</i> caf1 (F1) antigen expressed from plasmid pF51GA. The DNA construct can be used to transform human or animal gut colonizing microorganisms, specifically attenuated <i>Salmonella</i> typhimurium or <i>Salmonella</i> typhi. The transformed microorganisms can be used as live/attenuated vaccines which induce immune responses at mucosal surfaces. The vaccines provide protection against infection by <i>V. pestis</i> and are parenterally and orally active vaccines offering protection against bubonic and pneumonic plague.		
SQ	Sequence 151 AA:		
	Query Match 27.2%; Score 966; DB 14; Length 151;		
	Best Local Similarity 98.7%; Pred. No. 3_36e-60;		
	Matches 148; Conservative 2; Mismatches 0; Indels 0; Gaps		
Db	2	padltaatattatlvpararitykegapitimdngnidtelvlgtlqykgttsts 61	
Oy	44	ADLDTASTTATATLVEPARITYKEGAPITIMDNGNIDTELVLGTLTGYKGTTSTS 103	
Db	62	vnftdaagpmlylttsqsdnnhgfkttkvkgkdsrdflspkvngnlvgddvlatgs 121	
Oy	104	VNFTDAAGPMLYLTTSQSDNNHGFKTTKVKGKDSRDFDISPKVNGNLVGDDVLATGS 163	
Db	122	dfvvrsigsgklaagkytdavtvnsq 151	
Oy	164	dfvvrsigsgklaagkytdavtvnsq 193	



CC REFERENCE/DOCKET NUMBER: OPHD-01308
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 705-8410
 CC TELEFAX: (415) 397-8338
 CC INFORMATION FOR SEQ ID NO: 26:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 462 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE: 462 AA; 53932 MW; 1087243 CN;
 CC
 Query Match 4.2%; Score 150; DB 2; Length 462;
 Best Local Similarity 59.4%; Pred. No. 3.84e-02; 4; Indels 2; Gaps 1;
 Matches 19; Conservative 7; Mismatches 4;
 Db 1 MGHHHHHHHHHSSGHIEG-RHMASMRLS 30
 Qy 1 MGHHHHHHHHHSSGHIDDDKHMKISSVIA 32

RESULT 2 ID US-08-480-604A-26 STANDARD; PRT; 462 AA.
 XX DE Sequence 26, Application US/08480604A
 CC GENERAL INFORMATION:
 CC Patent No. 5736139
 Sequence 26, Application US/08480604A
 CC
 APPLICANT: KINK, JOHN A.
 CC
 APPLICANT: PADHVE, NISHA V.
 CC
 APPLICANT: FIRCA, JOSEPH R.
 CC
 APPLICANT: THALLEY, BRUCE S.
 CC
 APPLICANT: STAFFORD, DOUGLAS C.
 CC
 TITLE OF INVENTION: VACCINE AND ANITOXIN FOR TREATMENT AND
 PREVENTION OF C. DIFFICILE DISEASE
 CC
 TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
 CC
 NUMBER OF SEQUENCES: 32
 CC
 CORRESPONDENCE ADDRESS:
 CC
 ADDRESSEE: MEDLEN & CARROLL, LLP
 CC
 STREET: 220 MONTGOMERY STREET, SUITE 2200
 CC
 CITY: SAN FRANCISCO
 CC
 STATE: CALIFORNIA
 CC
 COUNTRY: UNITED STATES OF AMERICA
 CC
 ZIP: 94104
 CC
 COMPUTER READABLE FORM:
 CC
 MEDIUM TYPE: Floppy disk
 CC
 COMPUTER: IBM PC compatible
 CC
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CC
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CC
 CURRENT APPLICATION DATA:
 CC
 APPLICATION NUMBER: US/08/480,604A
 CC
 FILING DATE: 07-JUN-1995
 CC
 CLASSIFICATION: 424
 CC
 PRIOR APPLICATION DATA:
 CC
 APPLICATION NUMBER: US 08/422,711
 CC
 FILING DATE: 14-APR-1995
 CC
 PRIOR APPLICATION DATA:
 CC
 APPLICATION NUMBER: US 08/405,496
 CC
 FILING DATE: 16-MAR-1995
 CC
 PRIOR APPLICATION DATA:
 CC
 APPLICATION NUMBER: US 08/329,154
 CC
 FILING DATE: 25-OCT-1994
 CC
 PRIOR APPLICATION DATA:
 CC
 APPLICATION NUMBER: US 08/161,907
 CC
 FILING DATE: 02-DEC-1993
 CC
 PRIOR APPLICATION DATA:
 CC
 APPLICATION NUMBER: US 07/985,321
 CC
 FILING DATE: 04-DEC-1992
 CC
 PRIOR APPLICATION DATA:

RESULT 3 ID US-08-651-818A-21 STANDARD; PRT; 21 AA.
 XX DE Sequence 21, Application US/08651818A
 CC GENERAL INFORMATION:
 CC Patent No. 5948889
 Sequence 21, Application US/08651818A
 CC
 APPLICANT: de Boer, Piet A.J.
 CC
 APPLICANT: Hale, Cynthia A.
 CC
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING
 CC
 TITLE OF INVENTION: ANTIMICROBIALS
 CC
 NUMBER OF SEQUENCES: 25
 CC
 CORRESPONDENCE ADDRESS:
 CC
 ADDRESSEE: MEDLEN & CARROLL
 CC
 STREET: 220 Montgomery Street, Suite 2200
 CC
 CITY: San Francisco
 CC
 STATE: California
 CC
 COUNTRY: United States of America
 CC
 ZIP: 94104
 CC
 COMPUTER READABLE FORM:
 CC
 MEDIUM TYPE: Floppy disk
 CC
 COMPUTER: IBM PC compatible
 CC
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CC
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CC
 CURRENT APPLICATION DATA:
 CC
 APPLICATION NUMBER: US/08/651,818A
 CC
 FILING DATE:
 CC
 CLASSIFICATION: 530
 CC
 ATTORNEY/AGENT INFORMATION:
 CC
 NAME: Carroll, Peter G.
 CC
 REGISTRATION NUMBER: 32,837
 CC
 REFERENCE/DOCKET NUMBER: CASE-02249
 CC
 TELECOMMUNICATION INFORMATION:
 CC
 TELEPHONE: (415) 705-4410
 CC
 TELEFAX: (415) 397-8338
 CC
 INFORMATION FOR SEQ ID NO: 21:
 CC
 SEQUENCE CHARACTERISTICS:
 CC
 LENGTH: 21 amino acids
 CC
 TYPE: amino acid
 CC
 STRANDEDNESS: not relevant
 CC
 TOPOLOGY: not relevant
 CC
 MOLECULE TYPE: peptide

Query Match Similarity 4.1%; Score 144; DB 2; Length 21;
Best Local Similarity 94.4%; Pred. No. 9.19e-02; Mismatches 1; Indels 0; Gaps 0;

Match	Conservative	Mismatches	Indels	Gaps
Db	1 MGHHHHHHHHHHSQHIE 18	1 MGHHHHHHHHHHSQHIE 18	1 MGHHHHHHHHHHSQHIE 18	1 MGHHHHHHHHHHSQHIE 18
Qy	1 MGHHHHHHHHHHSQHID 18	1 MGHHHHHHHHHHSQHID 18	1 MGHHHHHHHHHHSQHID 18	1 MGHHHHHHHHHHSQHID 18

RESULT 4 ID US-08-405-496A-24 STANDARD; PRT; 23 AA.

RESULT 5 ID US-08-480-604A-24 STANDARD; PRT; 23 AA.

AC XXXXXX

AC XXXXXX

DE Sequence 24, Application US/08405496A

XX Sequence 24, Application US/08405496A

XX Sequence 24, Application US/08480604A

XX Sequence 24, Application US/08480604A

CC Patent No. 5919665

CC GENERAL INFORMATION:

CC APPLICANT: WILLIAMS, JAMES A.

CC TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM

CC NUMBER OF INVENTION: NEUROTOXIN

CC NUMBER OF SEQUENCES: 30

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: MEDLEN & CARROLL, LLP

CC STREET: 220 MONTGOMERY STREET, SUITE 2200

CC CITY: SAN FRANCISCO

CC STATE: CALIFORNIA

CC COUNTRY: USA

CC ZIP: 94104

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: FLOPPY DISK

CC COMPUTER: IBM PC COMPATIBLE

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/405,496A

CC FILING DATE: 16-MAR-1995

CC CLASSIFICATION: 424

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/329,154

CC FILING DATE: 25-OCT-1994

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/161,907

CC FILING DATE: 02-DEC-1993

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/985,321

CC FILING DATE: 04-DEC-1992

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/429,791

CC FILING DATE: 31-OCT-1989

CC ATTORNEY/AGENT INFORMATION:

CC NAME: INGOLA, DIANE E.

CC REGISTRATION NUMBER: 40,027

CC FILING DATE: 04-DEC-1992

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/429,791

CC FILING DATE: 31-OCT-1989

CC ATTORNEY/AGENT INFORMATION:

CC NAME: INGOLA, DIANE E.

CC REGISTRATION NUMBER: 40,027

CC FILING DATE: 04-DEC-1992

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/429,791

CC FILING DATE: 02-DEC-1993

CC ATTORNEY/AGENT INFORMATION:

CC NAME: INGOLA, DIANE E.

CC REGISTRATION NUMBER: 40,027

CC FILING DATE: 04-DEC-1992

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: OPHD-01308

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (415) 705-8410

CC TELEFAX: (415) 397-8338

CC INFORMATION FOR SEQ ID NO: 24:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 23 AMINO ACIDS

CC TYPE: AMINO ACID

CC STRANDEDNESS: UNKNOWN

CC TOPOLOGY: LINEAR

CC MOLECULE TYPE: PROTEIN

CC SEQUENCE 23 AA; 2741 MW; 2386 CN;

CC

Query Match 4.1%; Score 146; DB 2; length 23;

Best Local Similarity 79.2%; Pred. No. 6.87e-02;

CC CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
CC STREET: 8400 East Prentice Avenue, Suite #200
CC CITY: Englewood
CC STATE: Colorado
CC COUNTRY: USA
CC ZIP: 80111
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette 3.5 inch, 1.40 MB
CC MEDIUM TYPE: storage
CC COMPUTER: IBM COMPATIBLE
CC OPERATING SYSTEM: MS-DOS
CC SOFTWARE: WORD PERFECT 6.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/591,989
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX 49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
SEQUENCE LENGTH: 323
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
SQ SEQUENCE 323 AA; 33944 MW; 442207 CN;
Query Match 4.1%; Score 146; DB 2; Length 323;
Best Local Similarity 79.2%; Pred. No. 6.87e-02;
Matches 19; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
Db 17 MGHHHHHHHHHKGSGHSG--RHM 38
Qy 1 MGHHHHHHHHHKGSGHSGHIDDDKHM 24

RESULT 9 ID US-08-460-739-5 STANDARD; PRT; 168 AA.
AC XXXXXX
XX DT
XX Sequence 5, Application US/08460739
XX Sequence 5, Application US/08460739
CC Patent No. 5698415
CC GENERAL INFORMATION:
CC APPLICANT: Casels, Frederick J.
CC APPLICANT: Bell, Brian A.
CC TITLE OF INVENTION: Improved Methods for Production of
TITLE OF INVENTION: Antigens Under Control of Temperature-Regulated Promoters
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Glenna Heedricks
CC STREET: 9669 A Main Street
CC CITY: Fairfax
CC STATE: VA
CC COUNTRY: US
CC ZIP: 22031
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT-US95/07748A
CC FILING DATE: 16-JUN-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
NAME: HAILE, Ph.D.; LISA A.
REGISTRATION NUMBER: 38,347

CC FILING DATE: 20-APR-1995
CC CLASSIFICATION: 514
CC ATTORNEY/AGENT INFORMATION:
NAME: Handicks, Glenna M.
REGISTRATION NUMBER: 32,535
CC REFERENCE/DOCKET NUMBER: wof2
TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (703) 425-4250
CC TELEFAX: (703) 425-2767
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 168 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC ORIGINAL SOURCE:
CC ORGANISM: Cs3 protein
SQ SEQUENCE 168 AA; 17464 MW; 155638 CN;
Query Match 3.5%; Score 123; DB 1; Length 168;
Best Local Similarity 23.5%; Pred. No. 1.82e+00;
Matches 40; Conservative 48; Mismatches 72; Indels 10; Gaps 10;
Db 1 MLKIKYLLIGLISAMSYSLSAAGPTEKELAUNVSPALDAWTAPQDNLTLSNG-V 59
Qy 24 MKKISSV-IAIAALFGTIA-TANADLTASTATATLVEPARITYREGAPITIMDGNI 81
Db 60 -SNILVNGULTSNSIDTVSIASSTSVSDTSKNOT-VFAHETNSASFATI-ISTDNANI 116
Qy 82 DTEILVNGULTSQYKGTGS-TSVNFIDAGGDPMLLFTSQGNNHQPFTKVGKDSRDE 140
Db 117 TLD-KNAGNTIV-KTNGSQLQPLNPLKFTTVEGNEHVLVSGNKRNTIT 164
Qy 141 DISPKVNGENLVGDDWVLTGSDOFFVRSIGSKGG-LAAGKTDATVVT 189

RESULT 10 ID PCT-US95-07748A-2 STANDARD; PRT; 174 AA.
ID PCT-US95-07748A-2 STANDARD; PRT; 174 AA.
XX DT
XX Sequence 2, Application PC/TUS9507748A
XX DE Sequence 2, Application PC/TUS9507748A
CC Sequence 2, Application PC/TUS9507748A
CC GENERAL INFORMATION:
CC APPLICANT: The Regents of the University of California
CC TITLE OF INVENTION: CLONED Borrelia burgdorferi VIRULENCE
CC TITLE OF INVENTION: PROTEIN
CC NUMBER OF SEQUENCES: 8
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: Fish & Richardson P.C.
CC STREET: 4225 Executive Square, Suite 1400
CC CITY: La Jolla
CC STATE: California
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT-US95/07748A
CC FILING DATE: 16-JUN-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
NAME: HAILE, Ph.D.; LISA A.
REGISTRATION NUMBER: 38,347

Query Match 3.0%; Score 105; DB 1; Length 3248;
 Best Local Similarity 18.4%; Pred. No. 2.14e+01;
 Matches 69; Conservative 112; Mismatches 171; Indels 23; Gaps 21;
 Matches 69; Conservative 112; Mismatches 171; Indels 23; Gaps 21;

Db 2401 KLRARLEADEKKVTLQQLKESEHADLKGVERELETAARTNOEHAALEAENSKG 2460
 QY 295 RVKEFLESPNTQW-ELRAFMVNHFS-LTADRID-DI-LKVIDSMMNHGDARSKRE 350

Db 2461 EVETLKA--KIEGTMQSIRGLELDVVTIRSEKENLTNLQKEOERISELEIINSFE-NI 2517
 QY 351 ELAELTAELKIVSIVQAEINKHLSSGNTINHKSINLMDKNLYGTYDEEIKRASAEVKI 410

Db 2518 LQEKEQKVQMEKSSSTAMEMLOTLQKELNERVAALHNDQEACK-AKEQN LSS-QVECL 2574
 QY 411 LEKMPQTTIQV-DGSEKKIVSIKDFLGSENKRTGALGNLKNSSYNSYNKDNNELSHFATC- 468

Db 2575 ELEKAQIQLQGDEAK 2589
 QY 469 S-DKSRPLNDLVSQ 482

RESULT 15
 ID US-08-353-700-1 STANDARD; PRT; 3248 AA.
 XX AC XXXXXX
 XX DT
 DE Sequence 1, Application US/08353700
 XX Sequence 1, Application US/08353700
 CC Patent No. 5599819
 CC GENERAL INFORMATION:
 CC APPLICANT: YEN, TIMOTHY J.
 CC APPLICANT: RATTNER, JEROME B.
 CC TITLE OF INVENTION: NUCLEIC ACID ENCODING A
 CC TITLE OF INVENTION: TRANSIENTLY EXPRESSED KINETOCHORE PROTEIN,
 CC NUMBER OF SEQUENCES: 4
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: DANN, DORFMAN, HERSELL AND SKILLMAN
 CC STREET: 1601 MARKET STREET, SUITE 720
 CC CITY: PHILADELPHIA
 CC STATE: PA
 CC COUNTRY: USA
 CC ZIP: 19103-2307
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: FLOPPY DISK
 CC COMPUTER: IBM PC COMPATIBLE
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/353,700
 CC FILING DATE: 09-DEC-1994
 CC CLASSIFICATION: 435
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: REED, JANET E.
 CC REGISTRATION NUMBER: 36,252
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (215) 563-4100
 CC TELEFAX: (215) 563-4044
 CC INFORMATION FOR SEQ ID NO: 1:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 3748 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC HYPOTHETICAL: NO
 CC ANTI-SENSE: NO
 CC ORIGINAL SOURCE:
 CC ORGANISM: HUMAN
 CC
 *-SEQUENCE 3248 AA; 372207 MW; 51689535 CN;

Db 2226 ADEKKQHIAEKURE-REND-SLKDVNU-ERELQMSSEENQELVILDAENSKAEVET 2282
 QY 120 SDQNHNOPTTKVIGKDSRDFDISPKVNGENLVGDVYLATGSQDFVRSIGSKGKLA 179

Db 2283 LKIQEEMARSLKIFELDLVLRSEKENLTQIQQE-KQGQSLBDK-LIISFKSLLEKE 2340
 QY 180 GKV-TDAVIVTVSNEQEMIRAYQNPQHEDLEKVRVQELIGHGSVLEELVQVQKDN 238

Db 2341 QAEQIQLKESEKTAVEMLOTLQKELNERVAALHNDQEACK-AKEQN LSS-QVECL 2400
 QY 239 -IDISKIKDPRKODSEVFANRV- ITDIDIELLKKRILAYFLPEDTILKGG-HYDNLQNGIK 294

Db 2401 KLRARLEADEKKVTLQQLKESEHADLKGVERELETAARTNOEHAALEAENSKG 2460
 QY 295 RVKEFLESPNTQW-ELRAFMVNHFS-LTADRID-DI-LKVIDSMMNHGDARSKRE 350

Db 2461 EVETLKA--KIEGTMQSIRGLELDVVTIRSEKENLTNLQKEOERISELEIINSFE-NI 2517
 QY 351 ELAELTAELKIVSIVQAEINKHLSSGNTINHKSINLMDKNLYGTYDEEIKRASAEVKI 410

Db 2518 LQEKEQKVQMEKSSSTAMEMLOTLQKELNERVAALHNDQEACK-AKEQN LSS-QVECL 2574
 QY 411 LEKMPQTTIQV-DGSEKKIVSIKDFLGSENKRTGALGNLKNSSYNSYNKDNNELSHFATC- 468

Db 2575 ELEKAQIQLQGDEAK 2589
 QY 469 S-DKSRPLNDLVSQ 482

Db 295 RVKEFLESPNTQW-ELRAFMVNHFS-LTADRID-DI-LKVIDSMMNHGDARSKRE 350

Db 2461 EVETLKA--KIEGTMQSIRGLELDVVTIRSEKENLTNLQKEOERISELEIINSFE-NI 2517
 QY 351 ELAELTAELKIVSIVQAEINKHLSSGNTINHKSINLMDKNLYGTYDEEIKRASAEVKI 410

Db 2518 LQEKEQKVQMEKSSSTAMEMLOTLQKELNERVAALHNDQEACK-AKEQN LSS-QVECL 2574
 QY 411 LEKMPQTTIQV-DGSEKKIVSIKDFLGSENKRTGALGNLKNSSYNSYNKDNNELSHFATC- 468

Db 2575 ELEKAQIQLQGDEAK 2589
 QY 469 S-DKSRPLNDLVSQ 482

Search completed: Sat Nov 27 15:37:44 1999
 Job time : 27 secs.

FT comments)"
 PN WO9418318-A.
 PD 18-AUG-1994.
 PR 01-FEB-1993; US-013416.
 PR 30-DEC-1993; US-176100.
 PR 31-JAN-1994; US-18931.
 PA (UYNC-) UNIV NORTH CAROLINA.
 PI FOWKES DM, KAY BK;
 DR WPI; 94-21973934.
 PT identifying proteins or peptide(s) which bind a ligand - by
 PT screening a recombinant vector library expressing fusion proteins
 PT comprising a binding domain and an effector domain
 PS Disclosure; Page 35; 25pp; English.
 CC 070469 is a generic DNA sequence used to generate random TSAR peptide
 CC This generic formula can be represented as follows: X(TGC)(NNB)10-
 CC (TGC)(NNB)6Z(NNB)2(TGC)(NNB)14(TGCY). X and Y are flanking restriction
 CC sites (X is not the same as Y) that are not specified further. This
 CC generic sequences generates peptides that are cloverleaf in structure. Other
 CC generic sequences are shown in 070465-68. Other specific peptides
 CC concatenated heterofunctional proteins or peptides, comprising at least
 CC two functional regions - a binding domain with affinity for a ligand and
 CC a second effector peptide portion that is chemically or biologically
 CC active. They may further comprise a linker peptide between the 2 domains.
 CC The oligonucleotides are also designed so that the expressed peptide
 CC contains 2 or 4 cysteine residues positioned in, or flanking, the
 CC unpredicted or variant residues. These residues confer some degree of
 CC conformational rigidity to the peptides. The TSARs or compounds comprising
 CC a TSAR binding domain can be used in vivo to deliver a chemically or
 CC biologically active moiety, e.g. metal ion, radioisotope, peptide, toxin
 CC or enzyme, to the specific target or on the cell. They can also replace
 CC the function of macromolecules, e.g. monoclonal or polyclonal antibodies
 CC and therefore circumvent the need for complex methods of hybridoma
 CC formation or in vivo antibody production. The TSARs are easily
 CC characterised and have designed activity allowing direct and rapid
 CC detection in a screening process.
 SQ sequence 114 BP; 0 A; 4 C; 4 G; 4 T;

Query Match 2.3%; Score 36; DB 12; Length 114;
 Best Local Similarity 8.0%; Pred. No. 9.77e-07;
 Matches 9; Conservative 30; Mismatches 73; Indels 0; Gaps 0;
 Db 3 cnnbn 62
 Cp 229 CCATAATGTRATTGGAGCGCTTCTTATATGAGTGTGGCGGGCIGGTCAACAA 170
 Db 63 bnnbgnbn 114
 Cp 169 GAGTGTGGTGTGAGTGGTCTGGTAAATCTGCCGATTAGCTG 118

Search completed: Fri Apr 25 18:56:32 1997
 Job time : 147 secs.

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